

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Use of an enzyme mixture for the production of plant storage lipids containing polyunsaturated fatty acids

<130> 1

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 2425

<212> DNA

<213> Physcomitrella patens

<220>

<221> CDS

<222> (120)..(2135)

<223> Phospholipid:Diacylglycerin-Acyltransferase

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119

atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg
167

Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
1 5 10 15

cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac
215

Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
20 25 30

gaa tct tcc aaa tcc cac cat aag aaa tcg aac gga gga ggg aag tgg
263

Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp
35 40 45

tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc
311

Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
50 55 60

tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct
359

Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
 65 70 75 80
 cag tat gta acg gag cga atc acg ggt cct ttg cct gac ccg ccc ggt
 407
 Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly
 85 90 95
 gtt aag ctc aaa aaa gaa ggt ctt aag gcg aaa cat cct gtt gtc ttc
 455
 Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe
 100 105 110
 att cct ggg att gtc acc ggt ggg ctc gag ctt tgg gaa ggc aaa caa
 503
 Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
 115 120 125
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 551
 Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
 130 135 140
 gaa gtc tac aaa agg cct cta tgt tgg gtg gaa cac atg tca ctt gac
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 Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
 145 150 155 160
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 647
 Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
 165 170 175
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 695
 Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
 180 185 190
 gtg ctg att gct aac ctt gca cat att gga tat gaa gag aaa aat atg
 743
 Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
 195 200 205
 tac atg gct gca tat gac tgg cgg ctt tcg ttt cag aac aca gag gta
 791
 Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
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 839
 Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
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 887
 Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly

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Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro 260	265	270
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Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala 275	280	285
gtg atg aac att ggt gga cca ttt ctt ggt gtt cca aaa gct gtt gca 1031		
Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala 290	295	300
ggg ctt ttc tct gct gaa gca aag gat gtt gca gtt gcc aga gcg att 1079		
Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile 305	310	315 320
gcc cca gga ttc tta gac acc gat ata ttt aga ctt cag acc ttg cag 1127		
Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln 325	330	335
cat gta atg aga atg aca cgc aca tgg gac tca aca atg tct atg tta 1175		
His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu 340	345	350
ccg aag gga ggt gac acg ata tgg ggc ggg ctt gat tgg tca ccg gag 1223		
Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu 355	360	365
aaa ggc cac acc tgt tgt ggg aaa aag caa aag aac aac gaa act tgt 1271		
Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys 370	375	380
ggt gaa gca ggt gaa aac gga gtt tcc aag aaa agt cct gtt aac tat 1319		
Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr 385	390	395 400
gga agg atg ata tct ttt ggg aaa gaa gta gca gag gct gcg cca tct 1367		
Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser 405	410	415
gag att aat aat att gat ttt cga ggt gct gtc aaa ggt cag agt atc 1415		
Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile 420	425	430

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Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
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1511

Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
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1559

Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
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1607

Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
485 490 495

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1655

Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
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1703

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Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
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Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
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1895

Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
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1943

Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
595 600 605

cac tct ccg ccg gct aac ctg ttg gaa ggg cgc ggg acg cag agt ggt
1991

His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
610 615 620

gcc cat gtt gat atc atg gga aac ttt gct ttg atc gaa gat atc atg
2039

Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
625 630 635 640

agg gtt gcc gcc gga ggt aac ggg tct gat ata gga cat gac cag gtc
2087

Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
645 650 655

cac tct gcc ata ttt gaa tgg tcg gag cgt att gac ctg aag ctg tga
2135

His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
660 665 670

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2195

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<212> PRT

<213> Physcomitrella patens

<400> 2

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Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp
35 40 45

Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
 50 55 60
 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
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 Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly
 85 90 95
 Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe
 100 105 110
 Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
 115 120 125
 Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
 130 135 140
 Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
 145 150 155 160
 Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
 165 170 175
 Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
 180 185 190
 Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
 195 200 205
 Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
 210 215 220
 Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
 225 230 235 240
 Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
 245 250 255
 Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
 260 265 270
 Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala
 275 280 285
 Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
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 Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
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 Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
 325 330 335

His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
 340 345 350
 Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
 355 360 365
 Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
 370 375 380
 Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
 385 390 395 400
 Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
 405 410 415
 Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
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 Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
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 Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
 450 455 460
 Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
 465 470 475 480
 Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
 485 490 495
 Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
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 Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
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 Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
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 Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
 580 585 590
 Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
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625

630

635

640

Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
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